<110> Tryggvason, Karl
       Salo, Sirpa

<120> Use of antibodies to the gamma 2 chain of laminin 5 to inhibit tumor growth
and metastasis

<130> 02-1147-US

<150> 60/422,009
<151> 2002-10-29

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Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
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Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
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Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
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Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
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Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
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Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
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Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
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agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa    885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
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Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
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tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc    981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
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ctg gaa ggt gct ggt cta cgg atc aca gct ccc ttg atg cca ctt ggc    1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
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Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
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Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
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cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat    1173
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Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
        370                    375                    380

cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac    1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385          ·              390                    395                400

aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt    1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
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aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat    1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
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Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
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Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
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cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg    1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
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Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
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Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
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cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct    1701
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Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
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Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
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Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
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Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
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ttg gga aac act aac att cct gcc tca gac cac tac gtg ggg cca aat    2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
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ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac    2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
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Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
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 gag att  ggg agt ctg aac ttg  gaa gcc aat gtg aca  gca gat gga      3231
 Glu Ile  Gly Ser Leu Asn Leu  Glu Ala Asn Val Thr  Ala Asp Gly
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 gcc ttg  gcc atg gaa aag gga  ctg gcc tct ctg aag  agt gag atg      3276
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 agg gaa  gtg gaa gga gag ctg  gaa agg aag gag ctg  gag ttt gac      3321
 Arg Glu  Val Glu Gly Glu Leu  Glu Arg Lys Glu Leu  Glu Phe Asp
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 acg aat  atg gat gca gta cag  atg gtg att aca gaa  gcc cag aag      3366
 Thr Asn  Met Asp Ala Val Gln  Met Val Ile Thr Glu  Ala Gln Lys
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cga gcc aag acc cag atc aac agc caa ctg cgg ccc atg atg tca      3546
Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met Met Ser
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Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His Leu
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ctg gag aca agc ata gat ggg att ctg gct gat gtg aag aac ttg      3636
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Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln
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Ala Leu Glu Gln Gln
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65                  70                  75                  80


Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
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Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
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Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
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    290   295   300

Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305   310   315   320

Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
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Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
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Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
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Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
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Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
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Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
            405   410   415

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Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
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Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
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Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
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Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
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Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
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Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
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Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
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Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
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Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
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Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
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Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
    1010   1015   1020

Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
    1025   1030   1035

Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
    1040   1045   1050

Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
    1055   1060   1065

Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
    1070   1075   1080

Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr
    1085   1090   1095

Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Asp Gln Pro Leu
    1100   1105   1110

Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser
    1115   1120   1125

Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met Met Ser
    1130   1135   1140

Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His Leu
    1145   1150   1155

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Leu Glu  Thr Ser Ile Asp Gly  Ile Leu Ala Asp Val  Lys Asn Leu
    1160             1165             1170


Glu Asn  Ile Arg Asp Asn Leu  Pro Pro Gly Cys Tyr  Asn Thr Gln
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Ala Leu  Glu Gln Gln
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aggcgccggg cagcgacccc tgcagcggag acagagactg agcggcccgg caccgcc        117

atg cct gcg ctc tgg ctg ggc tgc tgc ctc tgc ttc tcg ctc ctc ctg      165
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
1               5                   10                  15

ccc gca gcc cgg gcc acc tcc agg agg gaa gtc tgt gat tgc aat ggg      213
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
            20                  25                  30

aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt      261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
        35                  40                  45

aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac      309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
    50                  55                  60

tgc gag aag tgc aag aat ggc ttt tac cgg cac aga gaa agg gac cgc      357
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
65                  70                  75                  80
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tgt ttg ccc tgc aat tgt aac tcc aaa ggt tct ctt agt gct cga tgt          405
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
                85                      90                  95

gac aac tct gga cgg tgc agc tgt aaa cca ggt gtg aca gga gcc aga          453
Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
                100                     105                 110

tgc gac cga tgt ctg cca ggc ttc cac atg ctc acg gat gcg ggg tgc          501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
            115                 120                 125

acc caa gac cag aga ctg cta gac tcc aag tgt gac tgt gac cca gct          549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
        130                 135                 140

ggc atc gca ggg ccc tgt gac gcg ggc cgc tgt gtc tgc aag cca gct          597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145                 150                 155                 160

gtt act gga gaa cgc tgt gat agg tgt cga tca ggt tac tat aat ctg          645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
                165                 170                 175

gat ggg ggg aac cct gag ggc tgt acc cag tgt ttc tgc tat ggg cat          693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
            180                 185                 190

tca gcc agc tgc cgc agc tct gca gaa tac agt gtc cat aag atc acc          741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
            195                 200                 205

tct acc ttt cat caa gat gtt gat ggc tgg aag gct gtc caa cga aat          789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
        210                 215                 220

ggg tct cct gca aag ctc caa tgg tca cag cgc cat caa gat gtg ttt          837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225                 230                 235                 240

agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa          885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
                245                 250                 255

ttt ctt ggg aat caa cag gtg agc tat ggg caa agc ctg tcc ttt gac          933
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
            260                 265                 270

tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc          981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
        275                 280                 285

ctg gaa ggt gct ggt cta cgg atc aca gct ccc ttg atg cca ctt ggc          1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
        290                 295                 300

aag aca ctg cct tgt ggg ctc acc aag act tac aca ttc agg tta aat          1077
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305                 310                 315                 320

gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat          1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
            325                 330                 335
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cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat      1173
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
        340             345             350

gga gaa tac agt act ggg tac att gac aat gtg acc ctg att tca gcc      1221
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
        355             360             365

cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt      1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
    370             375             380

cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac      1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385             390             395             400

aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt      1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
            405             410             415

aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat      1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
        420             425             430

tca ggg gat gag aat cct gac att gag tgt gct gac tgc cca att ggt      1461
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
        435             440             445

ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt      1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
        450             455             460

cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg      1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465             470             475             480

tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt      1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
            485             490             495

gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg      1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
            500             505             510

cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct      1701
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
        515             520             525

ggg aat tgt gac cgg ctg aca ggc agg tgt ttg aag tgt atc cac aac      1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
        530             535             540

aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac      1797
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545             550             555             560

cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac      1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
            565             570             575

ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt      1893
Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
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                 580                    585                      590
tgc aag cca gga ttt ggt ggc ccc aac tgt gag cat gga gca ttc agc    1941
Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
        595             600             605

tgt cca gct tgc tat aat caa gtg aag att cag atg gat cag ttt atg    1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
        610             615             620

cag cag ctt cag aga atg gag gcc ctg att tca aag gct cag ggt ggt    2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625             630             635             640

gat gga gta gta cct gat aca gag ctg gaa ggc agg atg cag cag gct    2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
                645             650             655

gag cag gcc ctt cag gac att ctg aga gat gcc cag att tca gaa ggt    2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
                660             665             670

gct agc aga tcc ctt ggt ctc cag ttg gcc aag gtg agg agc caa gag    2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
                675             680             685

aac agc tac cag agc cgc ctg gat gac ctc aag atg act gtg gaa aga    2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
        690             695             700

gtt cgg gct ctg gga agt cag tac cag aac cga gtt cgg gat act cac    2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705             710             715             720

agg ctc atc act cag atg cag ctg agc ctg gca gaa agt gaa gct tcc    2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
                725             730             735

ttg gga aac act aac att cct gcc tca gac cac tac gtg ggg cca aat    2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
                740             745             750

ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac    2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
        755             760             765

gtt gag tca gcc agt aac atg gag caa ctg aca agg gaa act gag gac    2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
        770             775             780

tat tcc aaa caa gcc ctc tca ctg gtg cgc aag gcc ctg cat gaa gga    2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785             790             795             800

gtc gga agc gga agc ggt agc ccg gac ggt gct gtg gtg caa ggg ctt    2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
                805             810             815

gtg gaa aaa ttg gag aaa acc aag tcc ctg gcc cag cag ttg aca agg    2613
Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
                820             825             830

gag gcc act caa gcg gaa att gaa gca gat agg tct tat cag cac agt    2661
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Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
        835             840                 845

ctc cgc ctc ctg gat tca gtg tct ccg ctt cag gga gtc agt gat cag    2709
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
        850             855                 860

tcc ttt cag gtg gaa gaa gca aag agg atc aaa caa aaa gcg gat tca    2757
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865             870                 875                 880

ctc tca agc ctg gta acc agg cat atg gat gag ttc aag cgt aca caa    2805
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
                885             890                 895

aag aat ctg gga aac tgg aaa gaa gaa gca cag cag ctc tta cag aat    2853
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
            900                 905                 910

gga aaa agt ggg aga gag aaa tca gat cag ctg ctt tcc cgt gcc aat    2901
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
            915                 920                 925

ctt gct aaa agc aga gca caa gaa gca ctg agt atg ggc aat gcc act    2949
Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
        930             935                 940

ttt tat gaa gtt gag agc atc ctt aaa aac ctc aga gag ttt gac ctg    2997
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945             950                 955                 960

cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc    3045
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
                965                 970                 975

tcc tac atc agc cag aag gtt tca gat gcc agt gac aag acc cag caa    3093
Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
                980                 985                 990

gca gaa aga gcc ctg ggg agc gct gct gct gat gca cag agg gca aag    3141
Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
            995                 1000                1005

aat ggg gcc ggg gag gcc ctg gaa atc tcc agt gag att gaa cag        3186
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
        1010                1015                1020

gag att ggg agt ctg aac ttg gaa gcc aat gtg aca gca gat gga        3231
Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
        1025                1030                1035

gcc ttg gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg        3276
Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
        1040                1045                1050

agg gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac        3321
Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
        1055                1060                1065

acg aat atg gat gca gta cag atg gtg att aca gaa gcc cag aag        3366
Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
        1070                1075                1080
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gtt gat  acc aga gcc aag aac  gct ggg gtt aca atc  caa gac aca      3411
Val Asp  Thr Arg Ala Lys Asn  Ala Gly Val Thr Ile  Gln Asp Thr
    1085              1090              1095

ctc aac  aca tta gac ggc ctc  ctg cat ctg atg ggt  atg tga          3453
Leu Asn  Thr Leu Asp Gly Leu  Leu His Leu Met Gly  Met
    1100              1105              1110

acccacaacc cacaaccttc cagctccatg ctccagggct ttgctccaga acactcacta   3513

tacctagccc cagcaaaggg gagtctcagc tttccttaag gatatcagta aatgtgcttt   3573

gtttccaggc ccagataact ttcggcaggt tcccttacat ttactggacc ctgtttttacc  3633

gttgctaaga tgggtcactg aacacctatt gcacttgggg gtaaaggtct gtgggccaaa   3693

gaacaggtgt atataagcaa cttcacagaa cacgagacag cttgggaatc ctgctaaaga   3753

gtctggcctg gaccctgaga agccagtgga cagttttaag cagaggaata acatcaccac   3813

tgtatatttc agaaagatca ctagggcagc cgagtggagg aaagcttgaa gagggggtta   3873

gagagaaggc aggttgagac tacttaagat attgttgaaa taattgaaga gagaaatgac   3933

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gtctgtgaag tcaagaatca cttgccggcc gggtgtggtg gctcacgcct gtaattctag   4053

cactttggga gactgaagcg ggtggatcac ccgaggtcag gagttgaaga ccagcctggc   4113

caacatggtg aaaccctgtc tctactaaaa gtacaaaaat tagctggatg atggtggtgg   4173

gcgcctgtaa ttccagctac tcaggagtct gaggcaggag aatcgcttga acccaggagg   4233

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cctaaaaaaa aaaaaaaaaa aaa                                           4316
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Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
            20                  25                  30


Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
        35                  40                  45


Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
    50                  55                  60


Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
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Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
              85   90   95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
              100   105   110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
              115   120   125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
    130   135   140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145   150   155   160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
              165   170   175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
              180   185   190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
    195   200   205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
    210   215   220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225   230   235   240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
              245   250   255

Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
              260   265   270

Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
    275   280   285

Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
    290   295   300

Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305   310   315   320

Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
                  325   330   335

Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
            340   345   350

Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
            355   360   365

Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
    370   375   380

Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385   390   395   400

Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
            405   410   415

Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
            420   425   430

Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
            435   440   445

Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
    450   455   460

His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465   470   475   480

Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
            485   490   495

Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
            500   505   510

Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
            515   520   525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
    530   535   540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545   550   555   560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
            565   570   575

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Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
            580             585             590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
        595             600             605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
    610             615             620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625             630             635             640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
            645             650             655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
            660             665             670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
        675             680             685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
    690             695             700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705             710             715             720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
            725             730             735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
            740             745             750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
        755             760             765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
    770             775             780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785             790             795             800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
            805             810             815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
            820             825             830
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Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
    835   840   845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
    850   855   860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865   870   875   880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
         885   890   895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
        900   905   910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
        915   920   925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
    930   935   940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945   950   955   960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
        965   970   975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
        980   985   990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
    995   1000   1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
    1010   1015   1020

Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
    1025   1030   1035

Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
    1040   1045   1050

Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
    1055   1060   1065

Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys

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            1070                    1075                    1080
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Val Asp  Thr Arg Ala Lys Asn  Ala Gly Val Thr Ile  Gln Asp Thr
        1085                    1090                    1095
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Leu Asn  Thr Leu Asp Gly Leu  Leu His Leu Met Gly  Met
        1100                    1105                    1110
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aattctgcca ggattgtgct tctggctaca agagagattc agcgagactg gggccttttg      60

gcacctgtat tccttgtaac tgtcaggggg gaggggcctg tgatccagac acaggagatt     120

gttattcagg ggatgagaat cctgacattg agtgtgctga ctgcccaatt ggtttctaca     180

acgatccgca cgacccccgc agctgcaagc catgtccctg tcataacggg ttcagctgct     240

cagtgattcc ggagacggag gaggtggtgt gcaataactg ccctcccggg gtcaccggtg     300

cccgctgtga gctctgtgct gatggctact ttggggaccc ctttggtgaa catggcccag     360

tgaggccttg tcagccctgt caatgcaaca gcaatgtgga ccccagtgcc tctgggaatt     420

gtgaccggct gacaggcagg tgtttgaagt gtatccacaa cacagccggc atctactgcg     480

accagtgcaa agcaggctac ttcggggacc cattggctcc caacccagca               530
```

```
<210>  6
<211>  177
<212>  PRT
<213>  Homo sapiens

<220>
<221>  misc_feature
<223>  Portion of Domain III of laminin gamma 2.
```

```
<400>  6
```

```
Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg
1               5                   10                  15
```

```
Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly
            20                  25                  30
```

```
Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro
        35                  40                  45
```

```
Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro His
    50              55                  60

Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser Cys
65              70                  75                  80

Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Pro
                85                  90                  95

Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly
            100             105             110

Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys Gln
        115             120             125

Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu
    130             135             140

Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr Cys
145             150             155             160

Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn Pro
            165             170             175

Ala
```

```
<210>   7
<211>   681
<212>   DNA
<213>   Homo sapiens

<220>
<221>   misc_feature
<223>   Complete domain III of laminin gamma 2

<400>   7
tgtatatgtc ctgttgggta caaggggcaa ttctgccagg attgtgcttc tggctacaag      60
agagattcag cgagactggg gccttttggc acctgtattc cttgtaactg tcaaggggga     120
ggggcctgtg atccagacac aggagattgt tattcagggg atgagaatcc tgacattgag     180
tgtgctgact gcccaattgg tttctacaac gatccgcacg accccgcag ctgcaagcca     240
tgtccctgtc ataacgggtt cagctgctca gtgattccgg agacggagga ggtggtgtgc     300
aataactgcc ctcccggggt caccggtgcc cgctgtgagc tctgtgctga tggctacttt     360
ggggacccct ttggtgaaca tggcccagtg aggccttgtc agccctgtca atgcaacagc     420
```

```
aatgtggacc ccagtgcctc tgggaattgt gaccggctga caggcaggtg tttgaagtgt    480

atccacaaca cagccggcat ctactgcgac cagtgcaaag caggctactt cggggaccca    540

ttggctccca acccagcaga caagtgtcga gcttgcaact gtaaccccat gggctcagag    600

cctgtaggat gtcgaagtga tggcacctgt gtttgcaagc caggatttgg tggccccaac    660

tgtgagcatg gagcattcag c                                              681
```

<210> 8
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2.

<400> 8

```
Cys Ile Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala
1               5                   10                  15


Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys
                20                  25                  30


Ile Pro Cys Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly
            35                  40                  45


Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys
        50                  55                  60


Pro Ile Gly Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro
65                  70                  75                  80


Cys Pro Cys His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu
                85                  90                  95


Glu Val Val Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys
                100                 105                 110


Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly
            115                 120                 125


Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn Val Asp Pro
        130                 135                 140


Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys
145                 150                 155                 160
```

```
Ile His Asn Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr
              165         170             175


Phe Gly Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys
              180         185             190


Asn Cys Asn Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly
              195         200             205


Thr Cys Val Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly
    210             215             220


Ala Phe Ser
225


<210>  9
<211>  9
<212>  PRT
<213>  Homo sapiens

<220>
<221>  misc_feature
<223>  N-terminal portion of domain III of laminin gamma 2.


<400>  9

Cys Ile Cys Pro Val Gly Tyr Lys Gly
1               5


<210>  10
<211>  41
<212>  PRT
<213>  Homo sapiens

<220>
<221>  misc_feature
<223>  C-terminal portion of domain III of laminin gamma 2.


<400>  10

Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu Pro Val
1               5               10              15


Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly Gly
              20              25              30


Pro Asn Cys Glu His Gly Ala Phe Ser
          35              40
```